Andrew R Wood

List of Publications by Year
in descending order

114 papers	30,195 citations	28736 57 h-index	24511 114 g-index
132 all docs	132 docs citations	132 times ranked	40143 citing authors

#	Article	IF	Citations
1	Understanding Factors That Cause Tinnitus: A Mendelian Randomization Study in the UK Biobank. Ear and Hearing, 2022, 43, 70-80.	1.0	7
2	Disease consequences of higher adiposity uncoupled from its adverse metabolic effects using Mendelian randomisation. ELife, 2022, 11, .	2.8	10
3	Babies of South Asian and European Ancestry Show Similar Associations With Genetic Risk Score for Birth Weight Despite the Smaller Size of South Asian Newborns. Diabetes, 2022, 71, 821-836.	0.3	3
4	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. Diabetes Care, 2022, 45, 772-781.	4.3	25
5	Simulated distributions from negative experiments highlight the importance of the body mass index distribution in explaining depressionâ€“body mass index genetic risk score interactions. International Journal of Epidemiology, 2022, 51, 1581-1592.	0.9	2
6	Fetal alleles predisposing to metabolically favorable adiposity are associated with higher birth weight. Human Molecular Genetics, 2022, 31, 1762-1775.	1.4	2
7	130â€… Does visual imagery vividness have a genetic basis? A genome-wide associa- tion study of 1019 individuals. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A51.1-A51.	0.9	0
8	Is disrupted sleep a risk factor for Alzheimerâ€™s disease? Evidence from a two-sample Mendelian randomization analysis. International Journal of Epidemiology, 2021, 50, 817-828.	0.9	31
9	Telomere length and risk of idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease: a mendelian randomisation study. Lancet Respiratory Medicine,the, 2021, 9, 285-294.	5.2	94
10	Sleep characteristics across the lifespan in 1.1â€‰million people from the Netherlands, United Kingdom and United States: a systematic review and meta-analysis. Nature Human Behaviour, 2021, 5, 113-122.	6.2	193
11	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 80-90.	1.8	5
12	Genetic determinants of daytime napping and effects on cardiometabolic health. Nature Communications, 2021, 12, 900.	5.8	136
13	Genetically defined favourable adiposity is not associated with a clinically meaningful difference in clinical course in people with type 2 diabetes but does associate with a favourable metabolic profile. Diabetic Medicine, 2021, 38, e14531.	1.2	1
14	Genetic predictors of participation in optional components of UK Biobank. Nature Communications, 2021, 12, 886.	5.8	106
15	Genetic Evidence for Different Adiposity Phenotypes and Their Opposing Influences on Ectopic Fat and Risk of Cardiometabolic Disease. Diabetes, 2021, 70, 1843-1856.	0.3	42
16	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
17	A genome-wide association study identifies 5 loci associated with frozen shoulder and implicates diabetes as a causal risk factor. PLoS Genetics, 2021, 17, e1009577.	1.5	23
18	Using Mendelian Randomisation methods to understand whether diurnal preference is causally related to mental health. Molecular Psychiatry, 2021, 26, 6305-6316.	4.1	26

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19	Higher adiposity and mental health: causal inference using Mendelian randomization. Human Molecular Genetics, 2021, 30, 2371-2382.	1.4	29
20	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
21	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. Diabetologia, 2021, 64, 2790-2802.	2.9	9
22	Mendelian randomization to investigate the link between TSH and thyroid cancer. Endocrine-Related Cancer, 2021, 28, L11-L14.	1.6	0
23	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. Nature Communications, 2021, 12, 5647.	5.8	61
24	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
25	Methods for quick, accurate and cost-effective determination of the type 1 diabetes genetic risk score (T1D-GRS). Clinical Chemistry and Laboratory Medicine, 2020, 58, e102-e104.	1.4	8
26	Effects of body mass index on relationship status, social contact and socio-economic position: Mendelian randomization and within-sibling study in UK Biobank. International Journal of Epidemiology, 2020, 49, 1173-1184.	0.9	42
27	Assessment of MTNR1B Type 2 Diabetes Genetic Risk Modification by Shift Work and Morningness-Eveningness Preference in the UK Biobank. Diabetes, 2020, 69, 259-266.	0.3	11
28	A single nucleotide polymorphism genetic risk score to aid diagnosis of coeliac disease: a pilot study in clinical care. Alimentary Pharmacology and Therapeutics, 2020, 52, 1165-1173.	1.9	17
29	Does Obesity Cause Thyroid Cancer? A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e2398-e2407.	1.8	40
30	Large Copy-Number Variants in UK Biobank Caused by Clonal Hematopoiesis May Confound Penetrance Estimates. American Journal of Human Genetics, 2020, 107, 325-329.	2.6	6
31	Clinical Features and Genetic Risk of Demyelination Following Anti-TNF Treatment. Journal of Crohn's and Colitis, 2020, 14, 1653-1661.	0.6	9
32	Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis in vitro. Human Molecular Genetics, 2020, 29, 1292-1309.	1.4	36
33	Quantification of the overall contribution of gene-environment interaction for obesity-related traits. Nature Communications, 2020, 11, 1385.	5.8	31
34	Genetic evidence that higher central adiposity causes gastro-oesophageal reflux disease: a Mendelian randomization study. International Journal of Epidemiology, 2020, 49, 1270-1281.	0.9	20
35	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	15.2	384
36	A Mendelian Randomization Study Provides Evidence That Adiposity and Dyslipidemia Lead to Lower Urinary Albumin-to-Creatinine Ratio, a Marker of Microvascular Function. Diabetes, 2020, 69, 1072-1082.	0.3	10

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37	Common maternal and fetal genetic variants show expected polygenic effects on risk of small- or large-for-gestational-age (SGA or LGA), except in the smallest 3% of babies. PLoS Genetics, 2020, 16, e1009191.	1.5	13
38	Mendelian randomization supports a causative effect of TSH on thyroid carcinoma. Endocrine-Related Cancer, 2020, 27, 551-559.	1.6	6
39	Mendelian randomization supports a causative effect of TSH on thyroid carcinoma. Endocrine-Related Cancer, 2020, 27, Z1.	1.6	0
40	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	5.8	117
41	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. BMJ: British Medical Journal, 2019, 365, l2327.	2.4	79
42	A genome-wide association study implicates multiple mechanisms influencing raised urinary albuminâ€“creatinine ratio. Human Molecular Genetics, 2019, 28, 4197-4207.	1.4	16
43	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. Gut, 2019, 68, 854-865.	6.1	84
44	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	5.8	417
45	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. PLoS Medicine, 2019, 16, e1002739.	3.9	144
46	Assessing the Pathogenicity, Penetrance, and Expressivity of Putative Disease-Causing Variants in a Population Setting. American Journal of Human Genetics, 2019, 104, 275-286.	2.6	158
47	Association of maternal circulating 25(OH)D and calcium with birth weight: A mendelian randomisation analysis. PLoS Medicine, 2019, 16, e1002828.	3.9	39
48	Genome-Wide Association Study of Microscopic Colitis in the UK Biobank Confirms Immune-Related Pathogenesis. Journal of Crohn's and Colitis, 2019, 13, 1578-1582.	0.6	32
49	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
50	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. Nature Communications, 2019, 10, 1100.	5.8	369
51	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. Nature Communications, 2019, 10, 1585.	5.8	189
52	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	9.4	250
53	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
54	OWE-16â€...Development and clinical validation of a genetic risk score for coeliac disease. , 2019, , .		0

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55	Mosaic Turner syndrome shows reduced penetrance in an adult population study. Genetics in Medicine, 2019, 21, 877-886.	1.1	88
56	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. American Journal of Human Genetics, 2019, 104, 157-163.	2.6	55
57	Using genetics to understand the causal influence of higher BMI on depression. International Journal of Epidemiology, 2019, 48, 834-848.	0.9	156
58	Common conditions associated with hereditary haemochromatosis genetic variants: cohort study in UK Biobank. BMJ: British Medical Journal, 2019, 364, k5222.	2.4	119
59	Development and Standardization of an Improved Type 1 Diabetes Genetic Risk Score for Use in Newborn Screening and Incident Diagnosis. Diabetes Care, 2019, 42, 200-207.	4.3	187
60	Response to Prakash et al.. Genetics in Medicine, 2019, 21, 1884-1885.	1.1	5
61	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. Diabetes, 2019, 68, 207-219.	0.3	72
62	Meta-analysis of genome-wide association studies for body fat distribution in 694Â649 individuals of European ancestry. Human Molecular Genetics, 2019, 28, 166-174.	1.4	752
63	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	1.4	156
64	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
65	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. Cell Reports, 2018, 23, 327-336.	2.9	76
66	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
67	Influence of cell distribution and diabetes status on the association between mitochondrial <scp>DNA</scp> copy number and aging phenotypes in the In<scp>CHIANTI</scp> study. Aging Cell, 2018, 17, e12683.	3.0	26
68	DNA methylation and inflammation marker profiles associated with a history of depression. Human Molecular Genetics, 2018, 27, 2840-2850.	1.4	46
69	Meta-analysis of genome-wide association studies for height and body mass index in â^¼700000 individuals of European ancestry. Human Molecular Genetics, 2018, 27, 3641-3649.	1.4	1,541
70	The Common HNF1A Variant I27L Is a Modifier of Age at Diabetes Diagnosis in Individuals With HNF1A-MODY. Diabetes, 2018, 67, 1903-1907.	0.3	12
71	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
72	Quantifying the extent to which index event biases influence large genetic association studies. Human Molecular Genetics, 2017, 26, ddw433.	1.4	40

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73	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
74	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. Diabetes, 2017, 66, 2296-2309.	0.3	102
75	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
76	Geneâ€“obesogenic environment interactions in the UK Biobank study. International Journal of Epidemiology, 2017, 46, dyw337.	0.9	159
77	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
78	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
79	Across-cohort QC analyses of GWAS summary statistics from complex traits. European Journal of Human Genetics, 2017, 25, 137-146.	1.4	18
80	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
81	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. PLoS ONE, 2017, 12, e0185083.	1.1	49
82	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
83	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.3	122
84	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
85	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
86	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	5.8	68
87	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. BMJ, The, 2016, 352, i582.	3.0	247
88	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.8	17
89	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.8	1
90	Variants in the FTO and CDKAL1 loci have recessive effects on risk of obesity and type 2 diabetes, respectively. Diabetologia, 2016, 59, 1214-1221.	2.9	65

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91	Genetic evidence that lower circulating FSH levels lengthen menstrual cycle, increase age at menopause and impact female reproductive health. Human Reproduction, 2016, 31, 473-481.	0.4	51
92	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
93	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	3.8	220
94	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308
95	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. Aging, 2016, 8, 547-560.	1.4	113
96	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
97	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
98	Biological interpretation of genome-wide association studies using predicted gene functions. Nature Communications, 2015, 6, 5890.	5.8	706
99	Cell Specific eQTL Analysis without Sorting Cells. PLoS Genetics, 2015, 11, e1005223.	1.5	115
100	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
101	Association Analysis of 29,956 Individuals Confirms That a Low-Frequency Variant at CCND2 Halves the Risk of Type 2 Diabetes by Enhancing Insulin Secretion. Diabetes, 2015, 64, 2279-2285.	0.3	24
102	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	1.4	8
103	Population genetic differentiation of height and body mass index across Europe. Nature Genetics, 2015, 47, 1357-1362.	9.4	227
104	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
105	Targeted Allelic Expression Profiling in Human Islets Identifies cis-Regulatory Effects for Multiple Variants Identified by Type 2 Diabetes Genome-Wide Association Studies. Diabetes, 2015, 64, 1484-1491.	0.3	31
106	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC Proceedings, 2014, 8, S2.	1.8	65
107	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
108	Quality control and conduct of genome-wide association meta-analyses. Nature Protocols, 2014, 9, 1192-1212.	5.5	398

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109	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
110	Another explanation for apparent epistasis. Nature, 2014, 514, E3-E5.	13.7	116
111	Imputation of Variants from the 1000 Genomes Project Modestly Improves Known Associations and Can Identify Low-frequency Variant - Phenotype Associations Undetected by HapMap Based Imputation. PLoS ONE, 2013, 8, e64343.	1.1	61
112	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
113	Allelic heterogeneity and more detailed analyses of known loci explain additional phenotypic variation and reveal complex patterns of association. Human Molecular Genetics, 2011, 20, 4082-4092.	1.4	61
114	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634